

HONORABLE MICHELLE L. PETERSON

UNITED STATES DISTRICT COURT
WESTERN DISTRICT OF WASHINGTON
AT SEATTLE

WILD FISH CONSERVANCY,

Plaintiff,

v.

BARRY THOM, in his official capacity as
Regional Administrator for the National
Marine Fisheries Service, *et al.*,

Defendants,

and

ALASKA TROLLERS ASSOCIATION,

Defendant-Intervenor.

Case No. 2:20-cv-00417-RAJ-MLP

DECLARATION OF GORDON
LUIKART, Ph.D.

I, Gordon Luikart, declare the following to which I am competent to testify under penalty of perjury of the laws of the United States:

1. I have been retained by Plaintiff Wild Fish Conservancy in this matter to evaluate the National Marine Fisheries Service's ("NMFS") proposal to increase hatchery production of Chinook salmon in Puget Sound, the Columbia River, and on the Washington Coast in an effort to compensate for impacts to the Southern Resident Killer Whale resulting from salmon harvests

LUIKART DECLARATION - 6
Case No. 2:20-cv-00417-RAJ-MLP

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1 in Southeast Alaska; specifically, I have been asked to provide expert opinions on the potential
2 genetic consequences to wild Chinook salmon from NMFS's proposal.

3 2. My current address is 41229 Haystack Mountain Lane, Polson, Montana 59860. I
4 have been retained to provide expert testimony on salmonid genetics by Plaintiff Wild Fish
5 Conservancy in this matter.

6 **PROFESSIONAL QUALIFICATIONS**

7 3. I have more than 30 years of professional experience researching and teaching at
8 the university level. Since 2000, I have specialized in research and teaching in the areas of
9 animal conservation, ecology, and population genetics/genomics.

10 4. From 1997-2000, I was a postdoctoral researcher in Europe working on large
11 (five-country) animal domestication and genetics projects funded by the European Union and
12 also NSF-NATO. I received a Ph.D. in Organismal Biology and Ecology in 1997 and an M.S. in
13 Zoology in 1992, both from the University of Montana (but including a year in Australia on a
14 Fulbright fellowship). I received a Bachelor of Science degree in Biology from Iowa State
15 University in 1988, with a minor in Animal Ecology.

16 5. Between 2005 and 2010 I have spent part of each year researching and teaching as
17 a visiting professor and senior research scientist with the Center for Investigation of Biodiversity
18 and Genetic Resources at the University of Porto, in Portugal. For the last ten years, I have spent
19 the majority of each year researching and teaching as a professor at the University of Montana's
20 Flathead Lake Biological Station. Courses I teach include advanced graduate level and
21 undergraduate level wildlife genetics/genomics classes, and conservation ecology.

22 6. I have conducted genetic research on fish and wildlife populations in several
23 different countries in addition to the United States and Portugal, including in Australia as a
24 Fulbright Fellow, and in France as a government scientist where I won the bronze medal as a top
25 researcher with the Centre National de la Recherche Scientifique. I have conducted research on a
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1 wide range of species, including goats and other ungulates, carnivores, fish, mussels, stoneflies,
2 and other aquatic species.

3 7. My research and teaching embrace various topics related to animal
4 genetics/genomics, including disease-diagnostics and transmission (via pathogen DNA testing),
5 population genetic modeling, captive and domesticated populations (including adaptation to
6 captivity), endangered and threatened species recovery, local adaptation, population size and
7 structure, effects of gene flow and hybridization (introgression) on individual fitness and
8 adaptation, and monitoring of the genetically effective population size and the effective number
9 of breeders using genetic markers in natural and managed populations.
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11 8. I have conducted numerous research investigations on these subjects. Serving as a
12 principal or co-principal investigator on more than 40 scientific research projects, my work has
13 produced chapters in six books, all relating to wildlife population genetics (one on animal
14 domestication), and over 100 scientific papers in peer-reviewed international journals; and I co-
15 authored a major text in 2007 on conservation genetics (the second edition of this book was
16 published in 2013 and the third edition commissioned for 2021; it contains continually-updated
17 sections directly relevant to salmon hatcheries and introgression effects on fitness and the
18 effective population size of wild stocks). In 2014 (and again in 2015-2018), I was recognized as
19 “one of the world’s most influential scientific minds” by Thomson Reuters, for publishing many
20 highly-cited over the past decade.

21 9. My recent research projects involved developing computer program simulators to
22 model landscape-level gene flow for aquatic species in complex river systems, and peer-
23 reviewed publications on RNA and DNA sequencing in trout and in wild and domestic
24 populations (including testing for adaptation to hatchery environments, and development of
25 novel estimators of introgression (hybridization) and also of the number of breeders (spawners
26 per year) from genetic marker data).
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1 10. My scholarship includes service on the editorial board of the journal
2 Environmental DNA and Conservation Biology, and as an associate editor for both Molecular
3 Ecology Resources and the Journal of Heredity.

4 11. I have served as an advisor for the Swan Ecosystem Center Native Fish
5 Committee and I have been a member of the American Fisheries Society, the Ecological Society
6 of America, the Society for Conservation Biology, the Society for the Study of Evolution, the
7 Wildlife Disease Association, and the Wildlife Society.

8 12. Attached hereto as Exhibit 1 is my curriculum vitae, which includes a list of all
9 peer-reviewed publications I have authored since 1996.

10 13. I have substantial familiarity with the genetics of animal domestication,
11 adaptation to captivity (e.g., hatchery environments), the effects of gene flow and introgression
12 on fitness and population persistence in fish and wildlife, local adaptation in salmonids, and
13 statistical and molecular empirical genomics.

14 14. I have not testified as an expert at trial during the last four years. I have testified
15 by deposition as an expert in the following cases: *McKenzie Flyfishers, et al. v. McIntosh, et al.*,
16 D. Or. No. 6:13-CV-02125-TC; *Native Fish Society, et al. v. National Marine Fisheries Service*,
17 D. Or. No. 3:12-cv-431-HA; and *Wild Fish Conservancy, et al. v. Nat'l Park Serv., et al.*, W.D.
18 Wash. No. 3:12-CV-05109-BHS.

19 15. I am being compensated for my work on this matter. My cost per hour is \$220.00,
20 and I have worked for approximately 14 hours at this point.

21 16. In addition to drawing upon my knowledge and experience, I have spoken with
22 Nick Gayeski, Ph.D. and have reviewed and considered the following documents in developing
23 my opinions expressed herein:

24 a. Allendorf, F.W., G. Luikart, and S. Aitken. 2013. Conservation and the
25 Genetics of Populations [Second Edition]. Wiley-Blackwell. Pp. 642; and also the Third Edition
26 which is submitted (in review);

b. Allendorf, F.W., and J.J. Hard, 2010. Human-induced evolution caused by unnatural selection through harvest of wild animals. *Proceedings of the National Academy of Sciences USA* 106: 9987-9994;

c. Amish, S.J., P.A. Hohenlohe, R.F. Leary, C. Muhlfeld, F.W. Allendorf, and G. Luikart. 2012. Next-generation RAD sequencing to develop species-diagnostic SNPs chips: An example from westslope cutthroat and rainbow trout. *Molecular Ecology Resources* 12:653–660. doi: 10.1111/j.1755-0998.2012.03157.x;

d. Araki, H., B. Cooper, and M.S. Blouin. 2007. Genetic effects of captive breeding cause a rapid, cumulative fitness decline in the wild. *Science* 318: 100–103. (doi:10.1126/science.1145621);

e. Araki, H., et al. 2008. Fitness of hatchery-reared salmonids in the wild. *Evolutionary Applications* 1: 342–355. (doi: 10.1111/j.1752-4571.2008.00026.x)

f. Barreto, R., D. Garcia de Leaniz C, Verspoor E, Sobolewska H, Coulson M. and Consuegra S. 2019. DNA methylation changes in the sperm of captive-reared fish: a route to epigenetic introgression in wild populations. *Molecular Biology and Evolution* 36: 2205-2211. (doi: 10.1093/molbev/msz135).

g. Baskett, M.L., and R.S. Waples. 2013. Evaluating alternative strategies for minimizing unintended fitness consequences of cultured individuals on wild populations. *Conservation Biology* 27:83–94;

h. Banks, M.A., N.M. Sard, K.G. O'Malley, D.P. Jacobson, M. Hogansen, K. Schroder, and M.A. Johnson. 2014. A genetic-based evaluation of the spring Chinook salmon reintroduction program above Cougar Dam, South Fork McKenzie River, 2007-2013. June 2014 Report. Prepared for U.S. Army Corps of Engineers, Portland District – Willamette Valley Project;

- i. Christie, M.R., M.L. Marine, R.A. French, and M.S. Blouin. 2012. Genetic adaptation to captivity can occur in a single generation. Proceedings of the National Academy of Sciences USA 109: 238–242;
- j. Christie, M.R., M.J. Ford, and M.S. Blouin. 2014. On the reproductive success of early generation hatchery fish in the wild. Evolutionary Applications. doi: 10.1111/eva.12183;
- k. Christie, M.R. et al. 2016. A single generation of domestication heritably alters the expression of hundreds of genes. Nature Communication 7: 10676 (doi: 10.1038/ncomms10676);
- l. ESA Recovery Plan for the White Salmon River Watershed, June 2013;
- m. ESA Recovery Plan for Lower Columbia River Coho Salmon, Lower Columbia River Chinook Salmon, Columbia River Chum Salmon, and Lower Columbia River Steelhead. June 2013;
- n. ESA Recovery Plan for Puget Sound Salmon Recovery Plan. January 2007;
- o. ESA Recovery Plan for Snake River Spring/Summer Chinook Salmon & Snake River Basin Steelhead, November 2017;
- p. 5-Year Status Review: Summary & Evaluation of Puget Sound Chinook Salmon, Hood Canal Summer-Run Chum Salmon, Puget Sound Steelhead, NMFS 2016;
- q. 5-Year Status Review: Summary & Evaluation of Lower Columbia River Chinook Salmon, Columbia River Chum Salmon, Lower Columbia River Coho Salmon, Lower Columbia River Steelhead, NMFS 2016;
- r. Hatchery and Genetic Management Plan for Kalama Falls Fall Chinook Hatchery Program (2014);
- s. Hess, M.A., C.D. Rabe, J.L. Vogel, J. J. Stephenson, D.D. Nelson, and S.R. Narum 2012. Supportive breeding boosts natural population abundance with minimal

negative impacts on fitness of a wild population of Chinook salmon. *Molecular Ecology* 21:5236–5250;

t. Hohenlohe, P.A., M.D. Day, S.J. Amish, M.R. Miller, N. Kamps-Hughes, M.C. Boyer, C.C. Muhlfeld, F.W. Allendorf, E.A. Johnson, and G. Luikart. 2013. Genomic patterns of introgression in rainbow and westslope cutthroat trout illuminated by overlapping paired-end RAD sequencing. Invited paper on next generation sequencing. *Molecular Ecology* 22: 3002–3013;

u. Hohenlohe, P.A., S.J. Amish, J. Catchen, F.W. Allendorf, and G. Luikart. 2011. RAD sequencing identifies thousands of SNPs for assessing hybridization in rainbow and westslope cutthroat trout. Invited paper, *Molecular Ecology Resources* 11: 117–122;

v. HSRG, 2009. HSRG White Paper No. 1: Predicted Fitness Effects of Interbreeding between Hatchery and Natural Populations of Pacific Salmon & Steelhead. Columbia River Hatchery Reform Project Final System-wide Report – Appendix A1. February 2009;

w. HSRG, 2015. Annual Report to Congress on the Science of Hatcheries - A report on the application of up-to-date science in the management of salmon and steelhead hatcheries in the Pacific Northwest;

x. Kibenge, M.J.T. et al. 2019 Piscine Orthoreovirus Sequences in Escaped Farmed Atlantic Salmon in Washington and British Columbia. *Virology Journal*, 16: 41.

y. Larson, D.L., Faisal, M., Tempelman, R.J., Yu, H., and Scribner, K.T. 2020. Effects of hatchery rearing density, handling, and nutrition on *Renibacterium salmoninarum* infection prevalence in juvenile Chinook salmon (*Oncorhynchus tshawytscha*). *J. Aquat. Anim. Health* 32:116-126. (doi: 10.1002/aah.10103;

z. Jonsson, B., Jonsson N. 2006. Cultured Atlantic salmon in nature: a review of their ecology and interaction with wild fish. *ICES Journal of Marine Science* 63: 1162e1181. (doi:10.1016/j.icesjms.2006.03.004);

1 aa. Lacy, R.C. 1993. VORTEX: A computer simulation model for Population
2 Viability Analysis. Wildlife Research 20:45-65.

3 bb. Lacy, R.C., R. Williams, E. Ashe, K.C. Balcomb III, L.J.N.
4 Brent, C.W. Clark, D.P. Croft, D. A. Giles, M. MacDuffee, P.C. Paquet. 2017. Evaluating
5 anthropogenic threats to endangered killer whales to inform effective recovery plans. Scientific
6 Reports 7: 1-12.

7 cc. Lacy, R.C., and J.P. Pollak. 2020. VORTEX: A Stochastic Simulation of the
8 Extinction Process. Version 10.4.0. Chicago Zoological Society, Brookfield, Illinois, USA.

9 dd. Lacy, R.C., P.S. Miller, and K. Traylor-Holzer. 2020. Vortex 10 User's
10 Manual. 1 April 2020 update. IUCN SSC Conservation Breeding Specialist Group, and Chicago
11 Zoological Society, Apple Valley, Minnesota, USA.

12 ee. Larocque, S.M., Johnson T.B., Fisk A.T. 2020. Survival and migration patterns
13 of naturally and hatchery-reared Atlantic salmon (*Salmo salar*) smolts in a Lake Ontario
14 tributary using acoustic telemetry. Freshwater Biology 65: 835-848.
15 (<https://doi.org/10.1111/fwb.13467>);

16 ff. Le Luyer, J., Laporte M., Beacham T.D., Kaukinen K.H., Withler R.E., Leong
17 J.S., Rondeau E.B., Koop B.F., Bernatchez L. 2017. Parallel epigenetic modifications induced by
18 hatchery rearing in a Pacific salmon. Proceedings of the National Academy of Sciences USA
19 114: 12964-12969. (doi: 10.1073/pnas.1711229114);
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21 gg. Losee, J.P., Kendall N.W., Dufault A. Changing salmon: An analysis of
22 body mass, abundance, survival, and productivity trends across 45 years in Puget Sound. Fish
23 and Fisheries 20: 934-951. (doi.org/10.1111/faf.12385);
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25 hh. Lynch, M., O'Hely M. 2001. Supplementation and the genetic fitness of
26 natural populations. Conservation Genetics 2: 363-378;

- ii. Milot, E., C. Perrier, L. Papillon, J.J. Dodson, L. Bernatchez. 2013. Reduced fitness of Atlantic salmon released in the wild after one generation of captive breeding. *Evolutionary Applications* 6: 472-485. (doi.org/10.1111/eva.12028);
- jj. G. J. Mordecai, K. M. Miller, E. Di Cicco, A.D. Schulze, K.H. Kaukinen, T.J. Ming, S. Li, A. Tabata, A. Tefferet. 2019. Endangered wild salmon infected by newly discovered viruses. *Elife* 8:e47615. (doi: 10.7554/eLife.47615);
- kk. Normandeau, E., Hutchings J.A., Fraser D.J., Bernatchez L. 2009. Population-specific gene expression responses to hybridization between farm and wild salmon. *Evolutionary Applications* 2: 489 – 503;
- ll. O'Sullivan, R.J., Aykanat T., Johnston S.E., Rogan G., Poole R., Prodöhl P.A., de Eyto, E., Primmer C.R., McGinnity P., Reed T.E. 2020. Captive-bred Atlantic salmon released into the wild have fewer offspring than wild-bred fish and decrease population productivity. *Proceedings Royal Society B*. 287:20201671. (doi: 10.1098/rspb.2020.1671);
- mm. Rocha de Almeida T., Alix M., Le Cam A., Klopp C., Montfort J., Toomey L., Ledoré Y., Bobe J., Chardard D., Schaerlinger B., Fontaine P. 2019. Domestication may affect the maternal mRNA profile in unfertilized eggs, potentially impacting the embryonic development of Eurasian perch (*Perca fluviatilis*). *PLoS One* 14:e0226878. (doi: 10.1371/journal.pone.0226878);
- nn. Ryman, N., and L. Laikre. 1991. Effects of supportive breeding on the genetically effective population size. *Conservation Biology* 5:325 – 329;
- oo. Theriault, V., G.R. Moyer, L.S. Jackson, M.S. Blouin, and M.A. Banks. 2011. Reduced reproductive success of hatchery Coho salmon in the wild: insights into most likely mechanisms. *Molecular Ecology* 20: 1860–1869.
- pp. Johnson, M.A., and T.A. Friesen. 2010. Spring Chinook salmon hatcheries in the Willamette Basin: Existing data, discernible patterns and information gaps. Oregon Department of Fish and Wildlife technical report to the U. S. Army Corps of Engineers, Portland

District. 87 pp. Available: https://nrimp.dfw.state.or.us/CRL/Reports/WHBOP/Johnson_and_Friesen_2010.pdf;

qq. Waples, R.S., G. Luikart, J.R. Faulkner, and D.A. Tallmon, 2013. Simple life history traits explain key effective population size ratios across diverse taxa. *Proc. Biol. Sci.* 280: doi: 10.1098/rspb.2013.1339;

rr. Waples, R.A., T. Antao, and G. Luikart. 2014. Effects of overlapping generations on linkage disequilibrium estimates of effective population size. *Genetics* 197: 769–780;

ss. Warheit, K.I. 2014. Measuring reproductive interaction between hatchery-origin and wild steelhead (*Oncorhynchus mykiss*) from northern Puget Sound populations potentially affected by segregated hatchery programs. Washington Department of Fish and Wildlife, Unpublished report, Olympia, WA;

tt. Wellband, K., et al. 2020. Environment-driven reprogramming of gamete DNA methylation occurs during maturation and influences offspring fitness in salmon. *bioRxiv* doi: <https://doi.org/10.1101/2020.11.25.396069>;

uu. Willoughby et al. 2018. Long-term demographic and genetic effects of releasing captive-born individuals into the wild. *Conservation Biology* 33: 377-388;

vv. Willoughby et al 2017. Captive ancestry upwardly biases estimates of relative reproductive success. *Journal of Heredity* 108: 583-587. doi: 10.1093/jhered/esx046; and

ww. Endangered Species Act (ESA) Section 7(a)(2) Biological Opinion and Magnuson-Stevens Fishery Conservation and Management Act Essential Fish Habitat Response, Consultation on the Delegation of Management Authority for Specified Salmon Fisheries to the State of Alaska, April 5, 2019 (“2019 SEAK BiOp”).

SUMMARY OF OPINIONS

17. In summary, it is my opinion that NMFS’s proposed increases in Chinook salmon hatchery production will appreciably contribute to the inability of numerous wild Chinook

1 salmon populations in the Puget Sound and the Columbia River ESUs to recover from their
2 threatened status under the Endangered Species Act (“ESA”) and will also reduce the likelihood
3 of their continued survival. The majority of rivers and streams in Puget Sound and the Lower
4 Columbia River already suffer high pHOS—the proportion of hatchery-origin spawners present
5 in the system—for Chinook salmon; the pHOS levels are significantly greater than those
6 necessary to prevent mal-adaptive hatchery-introgression and to help maintain the adaptive
7 capacity needed for the survival and recovery of wild ESA-listed Chinook salmon populations.
8 The levels of pHOS in the majority of these rivers thus pose a significant threat to the survival
9 and recovery of the wild Chinook populations. Similarly, pHOS levels in two Washington Coast
10 rivers for which recent data are available are also too high. NMFS’s proposal to increase
11 Chinook salmon hatchery production in an effort to offset impacts to Southern Resident Killer
12 Whales from salmon harvests will lead to even higher pHOS levels, thereby exacerbating
13 adverse genetic impacts to ESA-listed wild Chinook salmon populations.
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15 18. The reasons that high pHOS will likely cause long lasting harm, hindering or
16 preventing achievement of recovery objectives for threatened Chinook salmon populations and
17 evolutionary significant units (ESUs), include:

18 a. Hatchery-origin fish and offspring of hatchery-origin parents produce fish
19 that have lower fitness (ability to survive and reproduce) in the wild compared to wild native fish
20 (e.g., Allendorf et al. 2013; Christie et al. 2012, 2014, and 2016; Willoughby et al. 2017, 2018);

21 b. High pHOS results in the spreading of maladaptive genes from the
22 hatchery fish into the wild population via interbreeding in the wild, which will reduce local
23 adaptations;

24 c. The lower fitness and loss of local-adaptation could last for several
25 generations, causing potentially long-lasting harm (e.g., reduced viability and productivity) to the
26 native wild Chinook populations, which will likely hinder and may prevent the full recovery of
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the native populations and the entire ESU; further, lowered fitness and loss of local adaptation will likely persist for several generations following the elimination of any hatchery straying;

d. The gene flow (introgression) of maladaptive hatchery genes into wild populations will likely lower the future adaptive potential (i.e., the ability to adapt to environmental change such as climate change, habitat degradation, pollution, invasive species) of the wild populations of Chinook salmon (e.g., Christie et al. 2014); and

e. The introgression of maladaptive genes as well as the high pHOS (and straying of hatchery-origin fish) introduces substantial risks of spread of infectious disease pathogens into wild fish populations, which is of increasing concern given increased rates of spread of both native (endemic) and recently introduced European salmonid pathogens (e.g., viruses) into salmon populations in the Pacific Northwest (e.g., Miller et al. 2011; Mordecai et al. 2019; Kbenge et al. 2019; Larson et al. 2020).

**NMFS'S MITIGATION INITIATIVE FOR INCREASED HATCHERY PRODUCTION
INTENDED TO BENEFIT SOUTHERN RESIDENT KILLER WHALES**

19. NMFS's 2019 SEAK BiOp describes a funding initiative intended to increase prey available to Southern Resident Killer Whales, apparently in an effort to mitigate some of the impacts associated with salmon harvests in Southeast Alaska. 2019 SEAK BiOp 9–11, 227–28 (AR 47201–03, 47419–20). This mitigation action includes three components.

20. First, NMFS intends to distribute \$3.06 million per year for Puget Sound Chinook salmon "conservation" hatcheries. 2019 SEAK BiOp 10, 228 (AR 47202, 47420). This money would increase funding available for three existing Chinook salmon hatchery programs located on the Nooksack, Dungeness, and Stillaguamish Rivers and provide funding for an entirely new Chinook salmon hatchery program to be located somewhere in Hood Canal. *Id.* The 2019 SEAK BiOp indicates that the funding will likely result in modifications to the hatchery programs, which will most likely include increased production. 2019 SEAK BiOp 228 (AR 47420). No

1 further details are provided on this component of the mitigation package in the 2019 SEAK
2 BiOp.

3 21. Second, NMFS intends to distribute around \$31.2 million for habitat restoration
4 projects intended to benefit Chinook salmon populations in the same four Puget Sound
5 watersheds for which funding is provided for “conservation” hatchery programs: the Nooksack,
6 Dungeness, and Stillaguamish Rivers, and Hood Canal. 2019 SEAK BiOp 10, 227–28, 235–36
7 (AR 47202, 47419–20, 47427–28).

8 22. Third, NMFS proposes to provide funding to increase hatchery production of
9 Chinook salmon in an attempt to increase the prey available to Southern Resident Killer Whales
10 by 4% to 5% in areas deemed most important to the species. 2019 SEAK BiOp 10–11 (AR
11 47202–03). NMFS estimates that this mitigation component will cost no less than \$5.6 million
12 per year and will produce an additional 20 million Chinook salmon hatchery smolts annually.
13 2019 SEAK BiOp 11 (AR 47203). The 2019 SEAK BiOp indicates that “Five or six million
14 smolts should come from facilities in Puget Sound with the remainder from the Washington
15 Coast and Columbia River.” *Id.* No further details are provided on this component of the
16 mitigation package in the 2019 SEAK BiOp. *See* 2019 SEAK BiOp 240–41 (AR 47432–33).

17 23. This attempt to increase prey availability is far less than the increase needed to
18 reduce the decline in the Southern Resident Killer Whale (SRKW) population, according to
19 expert modeling (e.g., Lacy et al. 2017). Robert Lacy (of Lacy et al. 2017) is among the world’s
20 most experienced, respected, and sought-after modelers for conducting population viability
21 analysis (PVA) for the management and conservation of threatened species. Dr. Lacy has
22 conducted and applied PVA modeling with many management agencies and countries
23 (VORTEX; Lacy 1993; Lacy & Pollok 2020; Lacy et al. 2020).
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**POTENTIAL EFFECTS OF GENETIC INTERACTIONS BETWEEN
WILD AND HATCHERY SALMONIDS**

24. Hatchery domestication results from a process analogous to natural selection, but occurring under unnatural conditions (i.e., the hatchery rearing environment)—the individual fish (and genes) that are “selected” are those better adapted to life in unnatural conditions (high density, no predators, no disease or different disease, unnatural food, unnatural substrate and water flow, artificial spawning) (e.g., Allendorf and Hard 2010). The process results in reduced ability to avoid predation, reduced disease resistance, reduced ability to forage and spawn efficiently, etc. (e.g., De Mestral and Herlinger 2013), and release from the rigors of natural selection in the wild which permits genes that are maladaptive in the wild to attain high frequencies in the hatchery (Lynch and O’Hely 2001; HSRG 2009; Allendorf et al. 2013; Christie et al 2016).

25. This artificial selection pressure is strong; it results in rapid adaptation to captivity with a reduction of the ability to survive and reproduce effectively in the wild (e.g., Christie et al. 2012, 2016; Allendorf et al. 2013). The genes (or gene expression changes) that underlie these maladaptive traits will likely become fixed or increase to high frequency in hatcheries (even after only a few months of differential survival and development of embryos into fry and smolts).

26. Many of the genetic changes in captivity are likely heritable and transmittable to wild fish populations (e.g., Christie et al. 2012; 2014; 2016; Barreto et al. 2019; Wellband et al. 2020). Maladaptive genes (or gene expression profiles) from the hatchery fish can be transmitted to wild fish and thereby reduce the fitness of wild fish if the hatchery fish are allowed to spawn in the wild, as occurs when returning hatchery-produced adults stray onto the spawning grounds of local wild populations.

27. These domestication effects (i.e., adaptation to captivity) occur even when the hatchery fish are derived from the nearby local wild population and also when the hatchery operations regularly incorporate local wild fish into the hatchery broodstock. The negative fitness effects of hatchery fish derived from local wild populations on those same wild

populations are widely documented in the scientific literature (e.g., Araki et al., 2007a, b; Araki et al. 2009; Christie et al. 2011; Christie et al. 2012; Normandeau et al. 2009; Theriault et al. 2011; Grant 2011; Lorenz et al. 2012; O’Sullivan et al. 2020).

28. These negative effects are worse in the case of non-local, domesticated hatchery stocks, which is the case for many of the hatchery stocks in Puget Sound, the Washington Coast, and the Columbia River that will likely be the source of NMFS’s proposed hatchery mitigation measures at issue. This is because non-local fish are even less locally-adapted than local fish, which can reduce fitness locally in addition to the reduced fitness following hatchery-adaptation.

29. The Hatchery Science Review Group (“HSRG”) was founded and funded by Congress in 2000 to conduct reviews of salmonid (including steelhead) hatchery programs throughout the Pacific Northwest. As part of its review process, the HSRG developed criteria for the maximum number of “stray” hatchery-origin salmon present (and acceptable) on the spawning grounds of a wild salmon population (HSRG 2015). The criteria are based on two general factors: (a) the designated status of the wild populations as either a primary, contributing, or stabilizing population¹; and (b) the nature or kind of the hatchery program (e.g., isolated/segregated or integrated).

¹ The HSRG provides the following definitions for these population designations (HSRG Annual Report to Congress, On the Science of Hatcheries, 2015, page 34):

Population Designation Three population designations were defined by the Lower Columbia Fish Recovery Board (LCFRB 2004) and reflect the biological significance and the expected level of contribution of the population to recovery of the Evolutionarily Significant Unit (ESU) or Distinct Population Segment (DPS). The HSRG encourages co-managers to assign a population designation to each natural population associated with a hatchery program. The designation is a science-informed policy decision. The HSRG has recommended standards for hatchery influence (i.e., pHOS and PNI) for each designation.

Primary A population of high biological significance. Primary populations are critical to recovery of the ESU or DPS. They should meet the highest standards of viability.

Contributing A population of medium biological significance. Contributing populations are important to the diversity of the ESU or DPS. They should meet high standards of viability.

Stabilizing A population of lower biological significance than primary or contributing ones. Stabilizing populations should maintain current levels of viability.

30. An isolated/segregated hatchery program seeks to maintain genetic segregation (isolation) between the hatchery fish and the local wild populations. However, isolation is difficult or impossible to achieve such that gene flow (introgression) often occurs from hatchery fish into the wild fish populations (e.g., Seamons et al. 2012). Isolated hatchery programs commonly use a broodstock that was not derived from the local wild population(s) and they attempt to exclude wild fish from the adult fish used to supply broodstock for the hatchery. As a result, fish produced in isolated/segregated hatchery programs tend to become highly domesticated (e.g., Baskett and Waples 2012). These programs are primarily designed to provide returning adult salmon for harvest in ocean and/or in-river fisheries.

31. Integrated hatchery programs generally use broodstock developed from the local salmonid populations and regularly integrate returning wild adults into the hatchery's broodstock. Integrated hatchery programs are commonly used either for conservation purposes to aid in the recovery of ESA-listed populations or to provide fish for harvest while reducing the harmful impacts of adult fish that are not caught and that fail to return to the hatchery (strays).

32. The HSRG defined the metric pHOS, which stands for "proportion of hatchery-origin salmon" present on the spawning grounds with wild salmon. pHOS is defined as $HOR/(HOR + NOR)$, where HOR is the number of hatchery-origin spawners present on the spawning grounds and NOR is the number of natural-origin ("wild") spawners present. In other words, pHOS is the percentage of the total fish on the spawning grounds that are hatchery fish.

33. In its 2005-2009 Columbia River review, the HSRG described this definition of pHOS as census-pHOS ($pHOS_{census}$), and contrasted it with what it defined as "effective pHOS" ($pHOS_{eff}$). Effective pHOS is intended to modify (reduce) the census pHOS level by taking into account the lower wild-spawning fitness/success of hatchery-origin fish. That is, since it is known and accepted by fisheries geneticists that a hatchery-origin salmon spawning in the wild either with another hatchery-origin salmon or with a wild salmon will produce fewer returning adult offspring on average than a wild salmon spawning with another wild salmon, it is argued

that the level of actual flow of hatchery-origin genes to the wild population due to straying will be less than the level that would be estimated by simply using $\text{pHOS}_{\text{census}}$. Therefore, $\text{pHOS}_{\text{eff}} = \text{pHOS}_{\text{census}}$ multiplied by a correction factor (“cf”) that is less than 1.0.

34. Because of the significant harmful fitness consequences of genetic introgression into wild salmon populations by maladapted genes from hatchery fish, the HSRG adopted conservative standards for maximum permissible levels of pHOS for the hatchery programs (e.g., HSRG 2015). The recommended standards are intended to permit wild populations to be subjected to an acceptable level of some genetic and ecological harm from hatchery strays so as to enable isolated/segregated hatchery programs to continue to provide some hatchery fish for harvest. pHOS standards are lower (i.e., more restrictive) for isolated/segregated hatcheries than for integrated hatcheries because isolated hatcheries are likely to produce stronger adaptations to captivity and thus more harm to wild populations following gene flow into the wild (e.g., Basket and Waples 2013).

35. The pHOS standards recommended by the HSRG in its Columbia review for isolated/segregated hatchery programs affecting primary and contributing populations refer to effective pHOS (HSRG Columbia review, Final Systemwide Report, Part 3.1, page 29-30). For primary populations, the recommended maximum level of pHOS_{eff} is 5%; for contributing populations, the recommended maximum level of pHOS_{eff} is 10%. Since it is assumed that the correction factor, cf, is less than 1, the level of $\text{pHOS}_{\text{census}}$ corresponding to a pHOS_{eff} of 5%, for example, will be somewhat greater than 5%. The threshold levels of pHOS recommended by the HSRG in the Columbia review are also intended to apply to all Pacific salmon hatchery programs, and so are applicable to Puget Sound and Washington Coast salmon populations.

36. In a technical appendix to the Final Systemwide Report (Appendix A, page 17), the HSRG issued the following caution to emphasize the importance of keeping pHOS levels “low”: “The HSRG considers the preceding guidelines as minimal requirements for minimizing the genetic risks of hatchery programs to naturally spawning populations. For example, a value

of pHOS = 6% from a segregated hatchery population should not be viewed as exceeding the pHOS < 5% guideline by only 1%; on the contrary, a value of pHOS = 6% for a segregated hatchery population should be viewed as posing a significant, long-term genetic risk to the viability of a naturally spawning population if that potential level of gene flow continues unabated for many generations. Moreover, the aforementioned guidelines should not be interpreted as “benchmarks” or “goals”; rather, they should be interpreted in the context of their presentation here with respect to Figs. 3 through 10: that is, violation of any of those guidelines on a sustained basis over many generations will pose long-term genetic risks to the future viability of naturally-spawning populations.”

37. There is a significant problem with applying this pHOS standard to Chinook salmon hatchery programs. Except perhaps for steelhead, for which the reproductive success of hatchery fish relative to wild fish (“RRS,” for relative reproductive success) has been relatively well-studied, there are few good data and no scientific consensus on the appropriate value of a correction factor, *cf*, for Chinook salmon, other than it is highly likely less than 1. Thus, it is unknown how much greater than 5% or 10% the actual level of *census* pHOS could be in order for the *effective* pHOS not to exceed the 5% or 10% standard. The pHOS metric that is readily measured from spawning surveys and spawning escapement estimates is census pHOS, and this is the standard that should be used. This conclusion is supported by two complementary analyses, one by the HSRG and one by NMFS.

38. First, in its 2015 Annual Report to Congress on the Science of Hatcheries (HSRG 2015), the HSRG provided estimates of the long-term effects on fitness as a function of (effective) pHOS based on “recent studies and further analyses based on the Ford (2002) fitness model” (page 18 and Table 3, page 19).² What would be assumed as a “low” level of effective

² The Ford (2002) model is a genetic population model developed by geneticist Dr. Mike Ford, currently Director of the Conservation Biology Division of NMFS Northwest Fisheries Science Center, to estimate the fitness impacts on wild fish from hatchery fish spawning in the wild. This

pHOS of 2% resulted in the long-term fitness of the wild population being reduced to 85% of its level of fitness prior to straying. An effective pHOS of 5%, the level recommended for primary populations, resulted in long-term fitness being reduced to 62%—a very large and unacceptable 38% reduction in the productivity of the wild population. And pHOS of 10%, the level recommended for contributing populations, resulted in long-term fitness being reduced to only 20%. This lead the HSRG to conclude that “segregated (isolated) hatchery programs should be used with greater caution” and to state that “...the HSRG standard for segregated populations may be insufficient to safeguard the long-term viability of the affected naturally spawning primary and contributing populations (page 18).”

39. Second, in a biological opinion issued by NMFS dated May 29, 2015, on the effects of the operations of the Leavenworth National Fish Hatchery on ESA-listed threatened Upper Columbia River steelhead, NMFS explicitly cautioned against adjusting census pHOS by the relative reproductive success (RRS, correction factor) of hatchery-origin spawners, stating:

NMFS feels that adjustment of census pHOS by relative reproductive success (RRS) should be done very cautiously, not nearly as freely as the HSRG document would suggest. The basic reason is quite simple: the Ford (2002) model, the foundation of the HSRG gene flow guidelines, implicitly includes a genetic component of RRS. In that model, hatchery fish are expected to have RRS < 1.0 (compared to natural fish) due to selection in the hatchery. A component of reduced RRS of hatchery fish is therefore already incorporated in the model . . . Therefore, reducing pHOS values by multiplying by RRS will result in underestimating the relevant pHOS... (LNFH steelhead BiOp, page 88).

40. I agree with these concerns expressed by the HSRG and NMFS and believe that it is most appropriate to consider the HSRG’s recommended levels of pHOS for primary and contributing LCR Chinook populations to apply to census pHOS levels and not to (currently) incalculable levels of effective pHOS. However, this important issue is not particularly

model is the foundation for the model developed by the HSRG used to determine recommended levels of pHOS.

relevant/important here due to the current high (census) pHOS that far exceed HSRG recommendations.

THREATENED CHINOOK SALMON ESUs

41. There are several Chinook salmon ESUs listed as threatened species under the ESA that are potentially affected by NMFS's proposed hatchery increases intended to offset Southeast Alaska harvests.

42. The Puget Sound Chinook salmon ESU has been listed as a threatened species under the ESA since 1999. 64 Fed. Reg. 14,308 (March 24, 1999); *also* 50 C.F.R. § 223.102(e).

43. The Puget Sound Technical Recovery Team (PSTRT) identified 22 independent populations within the Puget Sound Chinook salmon ESU and separated them into five geographically similar major population groups. NMFS's most recent 5-Year Status Review (2016) provides:

To lower the extinction risk of the PS Chinook salmon ESU, all existing independent populations of Chinook salmon will need to improve from their current condition, and some will need to attain a low risk status. The PSTRT recommended that viable populations of Chinook salmon be spread throughout the region to minimize the risk of a catastrophic loss. The PSTRT also recommended that at least two to four populations in each of the five biogeographical regions of Puget Sound attain a low risk status. To minimize further loss of genetic diversity and life history characteristics of PS Chinook salmon, the PSTRT recommended at least one population from each major genetic and life history group in each of the five regions be viable, based on the historical patterns present within that region. (5-Year Status Review, p. 14).

44. With respect to the current condition of the Puget Sound Chinook salmon ESU, NMFS's most recent 5-Year Status Review provides:

All PS Chinook salmon populations are still well below the PSTRT planning ranges for recovery escapement levels. Most populations are also consistently below the spawner-recruit levels identified by the PSTRT as consistent with recovery. Across the ESU, most populations have declined in abundance since the last status review in 2011, and indeed, this decline has been persistent over the past 7 to 10 years. Productivity remains low in most populations. Hatchery-origin spawners are present in high fractions in most populations outside the Skagit

watershed, and in many watersheds the fraction of spawner abundances that are natural-origin have declined over time. (5-Year Status Review, p. 19).

45. The Lower Columbia River Chinook salmon ESU was listed as a threatened species in 1999. 64 Fed. Reg. 14,308 (March 24, 1999); *see also* 50 C.F.R. § 223.102(e).

46. The Willamette-Lower Columbia Technical Recovery Team (WLC TRT) has partitioned the Lower Columbia River Chinook salmon ESU into different major population groups, or strata, and developed biological criteria and methodologies at three different levels: evolutionary significant units, major populations groups or strata, and populations. NMFS's most recent 5-Year Status Review identifies the following "key points in defining a viable ESU/DPS":

- Every MPG or stratum that historically existed should have a high probability of persistence.
- Within each MPG or stratum, there should be at least two populations that have at least a 95 percent probability of persisting over a 100-year time frame.
- Within each MPG or stratum, the average viability of the populations should be 2.25 or higher, using the WLC TRT's scoring system. Functionally, this is equivalent to about half of the populations in the stratum being viable; a viable population is one whose persistence probability is high or very high.
- Populations targeted for viability should include those within the ESU/DPS that historically were the most productive ("core" populations) and that best represent the historical genetic diversity of the ESU/DPS ("genetic legacy" populations). In addition, viable populations should be geographically dispersed in a way that protects against the effects of catastrophic events.
- Viable populations should meet specific criteria for abundance, productivity, spatial structure, and diversity.

There are various ways to refer to extinction risk: as viability, persistence probability, extinction risk, or—at the population level—population status. The 2013 recovery plan frequently uses the terms "persistence probability" and "population status." Only populations with a persistence probability of 95 percent or higher over a 100-year time frame are considered viable. These populations have a population status of high or very high (NMFS 2013a). The 2013 Lower Columbia River Recovery Plan also includes detailed criteria for each of the five listing factors. (5-Year Status Review 2016).

47. With respect to the current condition of the Lower Columbia River Chinook salmon ESU, NMFS's most recent 5-Year Status Review provides:

The majority of the populations in this ESU remain at high risk, with low natural-origin abundance levels. Hatchery contribution to naturally-spawning fish remains high for a number of populations, and it is likely that many returning unmarked adults are the progeny of hatchery-origin parents, especially where large hatchery programs operate. While overall hatchery production has been reduced slightly, hatchery-produced fish still represent a majority of fish returning to the ESU. The continued release of out-of-ESU stocks: upriver bright (URB), Rogue River Select Area Bright (SAB) fall-run, Upper Willamette River spring-run, Carson Hatchery spring-run, and Deschutes River spring-run remain a concern. Relatively high harvest rates are a potential concern, especially for most spring-run and low abundance fall-run populations (NMFS 2012a). Although there have been a number of notable efforts to restore migratory access to areas upstream of dams, until efforts to improve juvenile passage systems bear fruition, it is unlikely that there will be significant improvements in the status of many spring-run populations. Alternatively, dam removals (i.e., Condit Dam, Marmot Dam, and Powerdale Dam) not only improve/provide access, but allow the restoration of hydrological processes that may improve downstream habitat conditions. Continued land development and habitat degradation in combination with the potential effects of climate change will present a continuing strong negative influence into the foreseeable future. In addition, coastal ocean conditions would suggest that recent outmigrant year classes will experience below average ocean survival with a corresponding drop in spawner abundance in the near term, depending on the duration and intensity of the existing situation. (5-Year Status Review, pp. 21–22).

48. The Upper Willamette River Chinook salmon ESU was also listed as threatened species in 1999. 64 Fed. Reg. 14,308 (March 24, 1999); *see also* 50 C.F.R. § 223.102(e).

49. The Snake River fall-run Chinook salmon ESU was listed as a threatened species in 1992. 57 Fed. Reg. 14,653 (April 22, 1992); *see also* 50 C.F.R. § 223.102(e).

OPINIONS ON HARMFUL IMPACTS TO THREATENED CHINOOK SALMON FROM NMFS'S PROPOSED MITIGATION HATCHERY PROGRAMS

50. I reviewed official PHOS data for Puget Sound, Washington Coast, and Lower Columbia River Chinook salmon reported on Washington Department of Fish and Wildlife's ("WDFW") Salmon Conservation Reporting Engine ("SCoRE") database, available at: <https://fortress.wa.gov/dfw/score/score/species/chinook>. These include rivers with hatchery

facilities that are most likely to be used for the increased production of hatchery Chinook salmon as proposed in the 2019 SEAK BiOp (cf. paragraphs 19 and 22 above).

51. The pHOS estimates in the majority of rivers are well in excess of levels recommended by the HSRG; the maximum levels that can be considered adequate to preserve the adaptive diversity and overall fitness of wild Chinook salmon populations. It is my professional opinion that even these levels (generally no greater than 5% nominal (census) pHOS) are likely too great. The table below provides a summary of the average values of pHOS since 2010 (generally 2010 to 2018 or 2019) for which data are available.

Table 1. Average Chinook salmon pHOS levels in rivers of Puget Sound, Washington Coast, and Lower Columbia River from WDFW's SCoRE website (accessed August 2020). Lower Columbia populations marked with a single asterisk (*) are designated a primary population in the Lower Columbia Chinook salmon Recovery Plan; populations marked with a double asterisk (**) are designated secondary population.

| Puget Sound: | Years | Hatchery Spawners | Total Spawners | Mean pHOS |
|--------------------------|--------------------|--------------------------|-----------------------|------------------|
| Dungeness | 2010-2019 Mean: | 348 | 457 | 75% |
| Nooksack Fall | 2010-2016 Mean: | 1098 | 1293 | 83% |
| NF Stillaguamish | 2010-2018 Mean: | 387 | 789 | 50% |
| Skykomish | 2010-2019 Mean: | 982 | 2806 | 34% |
| Snoqualmie | 2010-2019 Mean: | 258 | 1138 | 23% |
| Sammamish Fall | 2010-2019 Mean: | 1030 | 1139 | 89% |
| Cedar Fall | 2010-2019 Mean: | 281 | 1140 | 26% |
| Green Fall | 2010-2019 Mean: | 3009 | 4332 | 66% |
| Puyallup Fall | 2010-2019 Mean: | 1165 | 1716 | 67% |
| Nisqually Fall | 2010-2019 Mean: | 819 | 1505 | 48% |
| | | | | |
| Washington Coast: | | | | |

| | | | | |
|------------------------|--------------------|-------|-------|-----|
| Humptulips Fall | 2011-2019 Mean: | 1,686 | 4,816 | 35% |
| Wishka Fall | 2010-2019 Mean: | 65 | 486 | 13% |
| Lower Columbia: | | | | |
| Coweeman* | 2010-2019 | 146 | 876 | 17% |
| Big White Salmon | 2010-2019 | 246 | 833 | 30% |
| Elochaman-Skamokawa* | 2010-2018 Mean | 461 | 563 | 82% |
| Kalama Tule** | 2010-2018 Mean | 4763 | 6062 | 79% |
| Lower Cowlitz** | 2010-2018 Mean | 1069 | 3984 | 27% |
| Abernathy Creek* | 2010-2018 Mean | 129 | 147 | 88% |
| Mill Creek* | 2010-2018 Mean | 313 | 719 | 44% |
| Germany Creek* | 2010-2018 Mean | 206 | 233 | 89% |
| Toutle: Green | 2010-2018 Mean | 543 | 810 | 67% |
| South Fork Toutle* | 2010-2018 Mean | 116 | 200 | 58% |
| Upper Cowlitz | 2010-2016 Mean | 3375 | 3487 | 97% |
| Little White Salmon | 2010-2018 Mean | 212 | 468 | 45% |
| Wind River | 2010-2018 Mean | 849 | 1215 | 70% |
| Washougal* | 2010-2018 Mean | 1647 | 2457 | 67% |

52. As can be seen in Table 1, in Puget Sound rivers, pHOS values range from a low average value of 23% for the Snoqualmie River to a high average value of 89% in the Sammamish River. Five of these rivers (Dungeness, Nooksack, Stillaguamish (North Fork), Green and Puyallup) are among those at the top of the list of priority Chinook salmon stocks for Southern Resident Killer Whales listed in NMFS's 2019SEAK BiOp (Table 31) that are likely to provide the hatchery sources for the Puget Sound component of the proposed Chinook hatchery

mitigation releases). All five have current pHOS levels near 50% (NF Stillaguamish) or above 50% (the remaining four rivers).

53. The Lower Columbia also includes several rivers listed in NMFS's 2019 SEAK BiOp (Table 31) as high priority Chinook populations for Southern Residents, including the Kalama (average pHOS = 70.6%). All other rivers in the Lower Columbia River region listed in Table 1, with the exception of the Coweeman (average pHOS = 13.8%), have pHOS levels of 27% or greater.

54. All of the hatchery Chinook salmon that account for the pHOS levels for Puget Sound and Lower Columbia River populations identified in Table 1 above are hatchery adults that escaped all fisheries, failed to "home" back to the hatchery from which they were released as juveniles ("smolts"), and instead migrated to the spawning grounds of wild Chinook salmon, in ESUs (Puget Sound and Lower Columbia) in which Chinook salmon are listed as 'threatened' under the ESA. Thus, all of these un-caught fish were not preyed upon by Southern Resident Killer Whales. NMFS's proposal to increase hatchery production would similarly result in some proportion of additional hatchery Chinook salmon that escape fisheries and Southern Residents and do not return to the hatcheries, but instead stray onto spawning grounds, further increasing pHOS levels. This will further increase already dangerously high pHOS levels in all of these rivers. pHOS levels are 27% to more than 80% in these rivers, which is dangerously high according to the 2015 Report to Congress "On the science of Hatcheries", and other reports (HSRG 2009).

55. In the 2019 SEAK BiOp, NMFS does not discuss the likely fate of the adult Chinook produced from the proposed production of an additional 20 million hatchery smolts annually. This failure to discuss the likely fate is problematic. These fish will be subject to harvest under the 2019 Pacific Salmon Treaty as part of the Aggregate Abundance Based Management (AABM) fisheries (West Coast Vancouver Island (WCVI), North-Central British Columbia (NBC), and Southeast Alaska (SEAK)) before they are likely to be encountered by

1 (and accessible to) Southern Resident Killer Whales. In order to roughly estimate the magnitude
2 of additional straying onto wild spawning grounds by these hatchery Chinook salmon, I made the
3 following calculations.

4 56. Recent data (Losee et al. 2019) indicate that the average survival of Puget Sound
5 hatchery Chinook salmon from smolt release to adult return (smolt-to-adult survival, SAR) is
6 six-tenths of one percent (0.006). Hatchery fall Chinook salmon released from hatcheries in the
7 lower Columbia River have similarly low SAR values; e.g., for fishery years 2004 to 2013, the
8 Kalama Falls Fall Chinook Salmon hatchery program reported a SAR of 0.26% (0.0026)
9 (Hatchery and Genetic Management Plan for Kalama Falls Fall Chinook Hatchery Program,
10 Table 3.3.1.1, page 33 (2014)). Assuming that all 20 million proposed “mitigation” hatchery
11 Chinook salmon survive at this average rate (0.006), a total of 120,000 adult hatchery Chinook
12 salmon would be produced annually, on average. All of these fish would be subject to one or
13 more of the AABM fisheries under the 2019 Pacific Salmon Treaty before being accessible to
14 Southern Resident Killer Whales.
15

16 57. According to the 2019 SEAK BiOp (cf. paragraph 22 above), up to 6 million of
17 the 20 million smolts annually released would be released from Puget Sound hatcheries. The
18 remaining 14 million smolts produced annually (in Washington) would be released primarily
19 from lower Columbia River hatcheries, with the remainder being produced by hatcheries along
20 the Washington coast. The majority of Puget Sound Chinook salmon, both wild and hatchery-
21 origin, generally do not migrate to southeast Alaska, and are caught primarily in fisheries along
22 the West Coast of Vancouver Island, Canada (“WCVI” fisheries). Washington Coast and lower
23 Columbia River Chinook salmon generally migrate further north and are caught primarily in the
24 Southeast Alaska fisheries.
25

26 58. At a SAR of 0.006, an average of 36,000 adult Chinook salmon would be
27 produced annually from the additional 6 million hatchery smolts proposed to be released from
28 Puget Sound hatcheries, and an average of 84,000 adult Chinook salmon would be produced
29

1 from the additional 14 million hatchery smolts proposed to be released annually from hatcheries
2 in the Lower Columbia River and Washington coast.

3 59. According to the Pacific Salmon Treaty, the total allowable harvest (catch) in
4 AABM fisheries is tied to an “Abundance Index,” AI (2019 Pacific Salmon Treaty, Table 1, page
5 65). The index is based on the annual estimated total Chinook salmon abundance, with an AI =
6 1.0 corresponding to the average abundance in the baseline years of 1979 to 1982 of
7 approximately 1,235,020 Chinook salmon. If the annual abundance were equal to the baseline
8 value, the addition of 120,000 adult hatchery Chinook salmon from the proposed annual release
9 of 20 million smolts as “mitigation” ($20,000,000 \times 0.006 = 120,000$) would raise the AI from
10 1.0 to 1.1. When the AI = 1.0, the total allowable harvest in Southeast Alaska Treaty fisheries is
11 117,900, and the total allowable harvest in WCVI fisheries is 142,600 (2019 Pacific Salmon
12 Treaty Table 1, page 65). When the AI is 1.1, the total allowable harvest is 140,300 in the
13 Southeast Alaska fisheries, or 22,400 greater than when the AI is 1.0. An AI of 1.1 raises the
14 total allowable harvest in the WCVI fishery to 179,200, for an increase of 36,600 (ibid.).
15

16 60. Under this scenario, the WCVI fishery limit would be increased in an amount that
17 exceeds the additional 36,000 adult Chinook salmon produced from Puget Sound hatcheries as
18 mitigation in a supposed effort to benefit Southern Resident Killer Whales. Thus, the supposed
19 mitigation (release of 20,000,000 smolts) meant to support the killer whales would fail to provide
20 support.
21

22 61. Of the 84,000 adult Chinook salmon produced from annual releases at hatcheries
23 in the Lower Columbia River and on the Washington coast, 61,600 (84,000 less 22,400
24 additional Chinook salmon caught in the Southeast Alaska fisheries due to an increase in the
25 abundance index from 1.0 to 1.1, as explained above) would potentially be available to either
26 foraging Southern Resident Killer Whales or to freshwater spawning locations (hatchery
27 facilities or wild spawning grounds).
28

62. Based on average levels of pHOS in Lower Columbia River and Washington Coast rivers over the past decade as presented above, it is unlikely that the majority of the 61,600 hatchery adults would be consumed by Southern Resident Killer Whales. If, as a conservative estimate, it is assumed that 30,000 of these adult hatchery Chinook salmon escape harvest and predation by Southern Resident Killer Whales and return to rivers in the lower Columbia River Chinook salmon ESU, and further assume that half of these (15,000) would stray onto the spawning grounds of wild Chinook salmon, the potential increase in pHOS in the Lower Columbia River populations listed in Table 1 would be biologically significant. Averaged over all the Lower Columbia River Chinook salmon populations listed in Table 1, the current ESU-wide average pHOS is 0.65, or 65% (13,227 hatchery adults and 20,458 total (hatchery plus wild adults). Adding an additional 15,000 stray “mitigation” hatchery Chinook salmon to the 13,227 average stray hatchery adults would raise the average level of pHOS to 0.80, or 80% (28,227 hatchery adults and 35,458 total (hatchery plus wild) adults). Even if only 10,000 stray onto the spawning grounds of wild Chinook salmon, the potential increase in average pHOS would be to 76% (23,227 hatchery adults and 30,458 total (hatchery plus wild) adults). The current 65% pHOS is already above the pHOS acceptable under HSRG guidelines, and 76% to 80% is likely to cause further harm to wild ESA-listed Chinook.

CONCLUSION

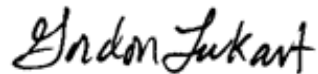
63. The Puget Sound Chinook salmon ESU and the Lower Columbia River Chinook salmon ESU are listed as threatened species under the ESA. According to NMFS’s most recent status reviews, most populations in the ESUs suffer low natural-origin abundance levels and have high fractions of hatchery spawners (pHOS). These high pHOS levels are likely contributing to the low productivity of the natural populations.

64. It is my opinion that the release of some 20 million additional hatchery Chinook salmon smolts from hatchery facilities in Puget Sound, the Columbia River, and on the Washington Coast will likely further increase pHOS levels and thereby further inhibit the

1 prospects for the continued survival, much less the recovery, of Chinook salmon populations in
2 the Puget Sound Chinook salmon ESU and the Lower Columbia River ESU.

3 Pursuant to 28 U.S.C. § 1746, I declare under penalty of perjury that the foregoing is true
4 and correct.

5 DATED this 24th day of February, 2021.

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10 _____
11 Gordon Luikart, Ph.D.
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EXHIBIT 1

Curriculum vitae

GORDON LUIKART

February 2021

CURRENT APPOINTMENTS:

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2014-current, Professor, Flathead Lake Biological Station, Division of Biological Sciences, University of Montana, USA
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2005-2010, Research Associate Professor, Organismal Biology and Ecology, University of Montana, USA
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2003-2005, Faculty Affiliate, University of Montana, USA
2004-2005, Research Scientist, Montana Conservation Science Institute (MOCSI), USA
2001-2005, Research Scientist (CR1), CNRS (Centre National Recherche Scientifique), France
(Officially on leave without pay until 2015)
2000-2001, CNRS, Research Fellow, Statistical and Population Genetics, France
1991-1992, Teaching Assistantships, Biological Station, U. of Montana (Aquatic Botany, Mammal Ecology)
1989-1995, Teaching Assistantships, U. of Montana (Genetics & Evolution, Conservation Genetics, Mammalogy, Ecology, Anatomy & Physiology),
1987, Research and Teaching Assistant, Sumilon University, Philippines (SCUBA diving & Marine Biology)
1986, Field Research Assistant, Virginia Polytech Institute (trapping & banding passerine birds)
1985-1986, Iowa Department of Natural Resources (gill-netting, radio-telemetry of fish, grouse, & otters)

ACADEMIC HONORS:

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Professor, Wildlife Biology Program and Systems Ecology Program, University of Montana, 2010-current
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Doctoral Research Fellowship, University of Montana, 1996
Fulbright Fellow, La Trobe Univ., Melbourne, Australia, 1994-95 (Genetics of endangered marsupials)

PROFESSIONAL ACTIVITIES: 2001-2004, Journal editorial board member for *Conservation Biology*
2003-2006, Journal associate editor for *Molecular Ecology Resources*
2009-2011, Associate editor for *Journal of Heredity*
2010-current, Member Swan Ecosystem Center Native Fish Committee
2010-current, Member IUCN Conservation Genetics Specialist group

TEACHING: 2018-current, Advanced Population Genetics, 3 credits (advanced undergrads, grad students)
2014-2017, Conservation Genetics, 3 credits (advanced undergrads and graduate students)
2010-current, Conservation Ecology, 3 credits (advanced undergrads), field course

.....2006-current, Population Genetic Data Analysis, 3 credits (grad students & postdocs)
<http://www.umd.edu/sell/cps/congen2018/>; www.popgen.net/congen2013
 2007-current, Population Genetics Seminar, 1 credit (undergrad and grad students)
 2007-2010 Genetics and Evolution, 3 credits (team taught, graduate students in NSF-IGERT)
 2006, 2010 Frontiers in Conservation Genetics, 2 credits (team taught)

SOCIETIES (Last five years): American Fisheries Society
 American Genetic Association
 Ecological Society of America
 Society for Conservation Biology
 Wildlife Society
 Freshwater Mollusk Conservation Society

BOOKS:

Allendorf, F.W. and **G. Luikart**. 2007. *Conservation and the Genetics of Populations*. Wiley-Blackwell. Pp. 642.
 Allendorf, F.W., **G. Luikart**, and S. Aitken. 2013. *Conservation and the Genetics of Populations* [2nd Edition]. Wiley-Blackwell. Pp. 642. 3rd edition to be published by Oxford University Press in 2021.

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PUBLICATIONS (in peer-reviewed journals): (*my students, ^students helped, **postdocs)
For some see: <http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=search&term=Luikart%20G>

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PUBLICATIONS in review or in prep: (*students, ^postdocs)

- *Moreno, N., *L. Howard, S. Relyea, J. Dunnigan, M. Boyer, ^M. Kardos, S. Glaberman, **G. Luikart**, and Y. Chiari. 2021. Gene expression estimates: Influence of sequencing library, sampling methods, tissue type, and harvest time in native fish. *Molec. Ecol. Resources*, In review.
- Miller, D. S. Amish, **G. Luikart**. In Prep. Invasive zebra mussel detection sensitivity is improved by orders of magnitude using a large-volume sampling method. In prep.
- Dahlquist, Z., Miller, D. Amish, S., **G. Luikart**. Environmental DNA testing detects invasive zebra

- mussels more often than microscopy from plankton tow net samples. In prep
- Amish, S.J., S. Bernall, P. DeHaan, M. Miller, S. O'Rourke, M.C. Boyer, C. Muhlfeld, S. Painter, R.F. Leary, and **G. Luikart**. Improved relatedness estimation, hybrid detection, and sex identification using a SNP-chip developed from next generation RAD sequencing in threatened bull trout. *In revision*.
- Hand, B.K., **G. Luikart**, S. Narum et al. Testing for genomic signatures of adaptation to captivity in Chinook salmon. In prep.
- Myers, B.J.E. et al. A new framework to test model-based biodiversity projections for policy formulation and implementation. *Biosciences*, Accepted pending revision.
- Hand, B.K., Raiford D.W., Landguth E.L., **G. Luikart**, J. Glassy. GARM: A machine learning algorithm for creating resistance maps in landscape genetics. In revision.
- Hand, B.K., Raiford D.W., Lowe W.H., Cross P.C., Anderson N.J., Chen S., and **Luikart G**. Confronting uncertainty in landscape genetics: a case study of elk connectivity in the Greater Yellowstone Ecosystem. In revision.
- *Cosart, T., S.J. Amish, S. Smith, A. Beja-Pereira, and **G. Luikart**. Next-generation sequencing of thousands of genes in divergent non-model taxa using exon capture. In prep.
- Jordan, S., S. Naderi, H. Reza, and **G. Luikart**. An improved Capra phylogeny from extensive sampling of wild populations and nuclear genes reveals origins and relationships of domestic and wild goats. In revision.

SELECTED GRANTS AND CONTRACTS AWARDED (RECENTLY):

- NASA-ROSES: Predicting the Spread of Aquatic Invasive Species Using Remote Sensing, Genetics, and Climate Modeling. \$740k. 2019-2022.
- NASA-ROSES (Ecological forecasting for conservation): Projecting effects of climate change on river habitats and salmonid fishes. \$750k. 2014-2018.
- NSF-DoB: (Dimensions of Biodiversity) - Predicting Biodiversity Vulnerability to Climate Change: Integrating Phylogenetic, Genomic, and Function Diversity in River Floodplains. \$2M. 2016-20.
- NSF-DEB: Evolutionary mechanisms influencing the spread of hybridization: genomics, fitness, and dispersal. \$600k. 2013-2017.
- MREDI (Montana University System): Development of autonomous chemical and biological instrumentation for environmental and industrial monitoring. M. DeGrandpre (PI), O. Berryman, C. Palmer, S. Amish, G. Luikart. \$1.4M, 2015-2017
- ARC (Australian Research Council) Linkage grant funding for a research project entitled "Genomics for persistence of Australia freshwater fish". P. Sunnucks et al. 2010-2017.
- NSF-ABI (Advances in Biological Informatics). ABI Development: The ECGen Pipeline: Improving genomics data analysis and inferences in ecological genomics. Pending resubmission.

SYNERGISTIC ACTIVITIES & OUTREACH:

- **Development of young scientists** – I have mentored >60 undergrad and grad students (& published with >30), mentored >6 postdocs, and helped occasional high school students in research projects. My lab group mentored 10 university undergrads from Montana and nationwide working on aquatic ecology projects for 2-20 weeks per student per summer in 2013-2016. I also teach several primary school classes each year about science, aquatic ecology, & conservation.
- **Organizing courses** - Population Genetic Data Analysis for graduate students, Portugal, 2006, 2008; for MS, PhD, postdocs and faculty, Montana, 2007, 2009, 2011, 2013-2020; e.g. www.popgen.net/congen2013; <http://www.umt.edu/ces/conferences/congen/>. Workshop/courses on invasive species detection with representatives from US Forest Service, US Geological Survey, Montana Fish Wildlife and Parks, and County Weed Districts.
- **Development of educational and fundraising videos (with collaborators)** – on "Conservation Genetics" <https://www.youtube.com/watch?v=MlaQnjibMq0>; and "Aquatic invasive species" prevention and eDNA detection <https://www.youtube.com/watch?v=ONXV2hhTp44&feature=youtu.be>; and citizen science "sampling of trout" training video: <https://www.youtube.com/watch?v=ymETcLLm5QY>; and on sampling wildlife to understand and control disease transmission <http://vimeo.com/33527913>; <http://www.gyeburcellosis.net/index.php>. See Brit Garner's CV (videographer).
- **Advising managers, agencies & specialist groups** (selected examples) – Montana Fish Wildlife and Parks cutthroat trout conservation committee; expert witness and consultant on hatcheries and wild salmon for Wild Fish Conservancy (WFC), Oregon and Washington state law firms 2011-present; Swan Valley Trout Restoration Program advisor; co-authored sections of MFWP bighorn sheep conservation action plan. IUCN Caprinae Specialists Group, taxonomy working group, 2001–2011. IUCN Genetics Specialist Group. GEO BON Genetics Composition working group, and GEO BON Species Populations working group.

- **Formal exchange program agreements** – Established between The University of Montana and The University of Porto, Portugal, 2007, 2009-present; and the National Zoological Gardens of South Africa 2018-present; Obtained funding for students and faculty from Montana to travel to and research in Portugal, 2006-present; South Africa 2018-2019.
- **Reviewer** – for the US National Science Foundation (proposals and panels), Genome Canada, and journals and agencies including: Nature Reviews Genetics, Proceedings of the Royal Society B, Science, Trends in Ecology & Evolution, Science. Advisory board member for the Journal Environmental DNA.